

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

**THIS PAGE BLANK (USPTO)**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

(without alignments)  
1394.265 Million cell updates/sec

### Scoring table

Xgapop	60.0	,	Xgapext	60.0
Ygapop	60.0	,	Ygapext	60.0
Fgapop	6.0	,	Fgapext	7.0
Delop	6.0	,	Delext	7.0

Searched: 16154066 seqs, 8097743376 residues

word size:

Total number of hits satisfying chosen parameters: 19385028

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODEL=fractal -3D -model

```

-O=cgml_1/USFTO.spool/US09865928.r/unat.06112002.160753.3581/app_query.fasta.1.327
-D=SE-1/CGM-fastasp -SUFFIX=oiliana.rst -MINMATCH=0.1 -LOPCPU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=lin40 -TRANS=human40.ccd -LIST=45
-DONTALIGN=200 -THR SCORE=quality -THR MIN=4 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc
-NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USR=US09865928.ecgn.1.1.1716.etunat.06112002.160753.3581 -NCPU=6 -ICPU=3
-NO_XLRY NO_MMAB -LARGESUBSET -NES_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THEADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

```

Database :

1:	em_estbda.*
2:	em_estbda.*
3:	em_estlin.*
4:	em_estlin.*
5:	em_estlov.*
6:	em_estpl.*
7:	em_estro.*
8:	em_hnc.*
9:	gb_estli.*
10:	gb_estc.*
11:	gb_hnc.*
12:	gb_estc.*
13:	gb_estc.*
14:	gb_estc.*
15:	em_estun.*
16:	em_estom.*
17:	gb_gss.*
18:	em_gss_hum.*
19:	em_gss_inv.*
20:	em_gss_pln.*
21:	em_gss_vrt.*
22:	em_gss_fun.*
23:	em_gss_mam.*
24:	em_gss_mus.*
25:	em_gss_other.*
26:	em_gss_pro.*
27:	em_gss_rod.*

Result	Score	Query	Length	ID	Description
No.		Match		DB	
1	190	100.0	807	12	BG184448
2	181	95.3	691	10	AM582253
3	153	80.5	768	12	BG194960
4	148	77.9	822	12	BG219307
5	130	68.4	789	12	BG221275
6	125	65.8	823	12	BG188390
7	123	64.7	837	12	BG216071
8	112	58.9	447	13	BG982234
9	110	57.9	594	10	AM469181
10	97	51.1	777	12	BG217799
11	81	42.6	698	12	BG375244
12	78	41.1	871	12	BG198917
13	74	38.9	807	12	BG187692
14	70	36.8	415	14	BQ084432
15	65	34.2	482	14	BM773483
16	60	34.2	480	9	AI697014
17	61	32.1	268	12	BG184955
18	55	28.9	529	13	BG432955
19	55	28.9	758	12	BG198969
20	54	28.4	810	12	BG211267
21	50	26.3	398	14	BM773482
22	50	26.3	428	9	AI830044
23	50	26.3	508	12	BF375243
24	26	3	777	9	AUI38880
25	49	25.8	558	9	AI799626
26	45	23.7	846	12	BG202006
27	41	21.6	855	12	BG204090
28	39	20.5	243	12	BG216765
29	39	20.5	565	14	BQ552730
30	39	20.5	2721	11	AK016573
31	37	19.5	639	14	BM978431
32	36	18.9	359	14	BM755790
33	34	17.9	340	13	BG977333
34	33	17.4	559	12	BF378919
35	32	16.8	829	12	BG201350
36	31	16.3	376	12	BG849364
37	31	16.3	491	12	AM913564
38	31	16.3	563	14	BM837518
39	28	14.7	385	10	AM469177
40	27	14.2	324	10	AM869793
41	27	14.2	327	10	BE183571
42	25	13.2	303	12	BG205109
43	23	12.1	652	9	AV226010
44	18	9.5	191	9	AA371314
45	16	8.4	361	10	BE002927
					BG184448
					RST3374
					A
					AM582253
					QV4-ST021
					BG194960
					RST14018
					BG219307
					RST39061
					BG221275
					RST41079
					BG188390
					RST2815
					A
					BG216071
					RST35885
					BG982234
					CM4-CN008
					AM469181
					hc78f11.x
					BG217799
					RST37513
					BF375244
					QV4-ST021
					BG198917
					RST18188
					BG187692
					RST6558
					A
					BQ084432
					K-EST0149
					BM773483
					K-EST0057
					AI697014
					wc76h09.x
					AM434895
					RST3889
					A
					BG432955
					1IE18B4
					BM198969
					RST18241
					BG211267
					RST18969
					BM773482

## ALIGNMENTS

RESULT 1	
BG184448	
LOCUS	BG184448 807 bp mRNA linear EST 21-APR-2001
DEFINITION	R53J374 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION	BG184448
VERSION	BG184448.1 GI:13706135
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 807)
AUTHORS	Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran.R., Whittington,J, , Derner,L., Costanzo,D., McElligott,K., Boozee,S., Mays,R., Smith

TITLE  
JOURNAL MEDLINE  
COMMENT

CONTACT: Scott J. Cain

Address: 3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scalcath@ersys.com

High quality sequence stop: 499.

## FEATURES

source

1. 807

/db\_xref="taxon:9606"

/clone\_lib="Athersys RAGE Library"

/cell\_line="HT1080"

/note="See 'Creation of Genome-Wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 211 a 195 c 178 g 222 t 1 others

ORIGIN

## Alignment Scores:

pred. No.: 2.63e-192 Length: 807  
Score: 190.00 Matches: 190  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG184448 (1-807)

QY 1 MetMetAsnPhcGlnPropSerLysAlaTrpArgAlaSerGlnMetMetTrpPhe 20  
DB 85 ATGATGAATTTCCAGCCTCGAGCAAAAGCCTGGGGCCCTCACAGATGACTTTTTC 144  
QY 21 IlePheLeuLeuPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 40  
DB 145 ATCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 204  
QY 41 TrpArgLeuLysProSerAlaAspGlyProPheArgGlyLeuProLeuPheIleHis 60  
DB 205 TGGGATTTGAAGCCTTCAGCTGAGCTGGCCCTTTTCTGAGGCTCTGCTCTTCTTCTT 264  
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTrpLeuTrpValValTrp 80  
DB 265 TCCATCTACAGCTGGATCGACACCTTAAGTACAGGCGCTGGCTGCTGGTGGTGG 324  
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100  
DB 325 ATCTATCGGAACCTCAATGGAAGTGTGCACTTCTTCTTCTTCTTCTTCTTCTTCTT 384  
QY 101 IleIleThrTrpLeuTrpTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120  
DB 385 ATATCTACCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 444  
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140  
DB 445 CATGAGCAGATCATATATGAGGCAAAAGATTAATGTTCTGTATGAAAATTGATCAAG 504  
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160  
DB 505 CTCGACAGATATGAGAAGAAAGCAACCCAGCTCACTTCTTCTTCTTCTTCTTCTTCTT 564  
QY 161 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 624  
DB 565 GAGCAACAAGGCTTTTGGCATTTGGGGGACATGATGGCAGTCTTGACTTGGCATTTAGA

QY 181 ArgSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 190  
DB 625 AGATCAGTTCAAGAGGATATCCAGGGCC 654

## RESULT 2

LOCUS

DEFINITION

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

AM582253

## FEATURES

source

1. 691

/db\_xref="taxon:9606"

/clone\_lib="ST0212"

/dev\_stage="Adult"

/note="Organ: Stomach; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESPES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 179 a 167 c 157 g 188 t

ORIGIN

## Alignment Scores:

pred. No.: 9.22e-183 Length: 691  
Score: 161.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 95.26% Indels: 0  
DB: 10 Gaps: 0

US-09-895-298a-83 (1-190) x AM582253 (1-691)

QY 10 AlaTrpArgAlaSerGlnMetMetTrpPhePheIlePheLeuLeuPhePheProSerPhe 29  
DB 53 GCTGGGGGGGCGTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 112  
QY 30 ThrGlyValLeuGlySerThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCys 49  
DB 113 ACCGGGCTCTTGTGACCCCGGCATCACCATGTGGAGATTGAAGCTTACGCTGACTGT 172  
QY 50 GlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeu 69  
DB 173 GGCCCTTTTGGAGGCTGCTCTTTCATTCATTCATTCATTCATTCATTCATTCATTCAT 232

QY 70 SerThrArgProGlyTyrLeuTrpValValTriLeuTyrArgAsnLeuIleGlySerVal 89  
|||||  
Db 233 AGTACAGCGCCCTGGCTACCTGGTGGTGGATCTATCGAACCCTATTGGAAGTGG 292  
QY 90 HisPhePhePheIleLeuThrIleValLeuIleIleThrTyrLeuTyrTrpGlnIle 109  
|||||  
Db 293 CACTTCTTTTCATCCTCACCCTCATTTGTCTAATCATCATCCTATCTTACTCGGAGATC 352  
QY 110 ThrGlnGlyArgValIleMetIleArgLeuHisGlnGlnIleIleAsnGlnGlyLys 129  
|||||  
Db 333 ACAGAGGAGAGAGATTTATGATTAAGCGCTCCATGACAGATCATTTATATAGGCGCAA 412  
QY 130 AspLysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsn 149  
|||||  
Db 413 GATAAAATGTTCTGATGAAAAATGATTCACAGCTGCAGAGATATGAGAGAAGAAACCAAC 472  
QY 150 ProSerSerLeuValLeuGluArgArgGluValGlnGlnGlnGlyPheLeuHisLeuGly 169  
|||||  
Db 473 CCCACTCATCTGTCTGTGAAAGAGAGGTGAGCAACAAGGCTTTTTCATTTGGGG 532  
QY 170 GluHisAspGlySerLeuAspLeuArgSerArgArgSerValGlnGlnGlnProArg 189  
|||||  
Db 533 GAACTATGATGGCATGCTTACTTGCATCTAGAAATCATGTTCAAGAAAGTATCCAAAG 592  
QY 190 Ala 190  
|||  
Db 593 GCC 595  
RESULT 3  
Bg194960 768 bp mRNA linear EST 21-APR-2001  
LOCUS Bg194960  
DEFINITION RST14018 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION Bg194960  
VERSION Bg194960.1 GI:13716535  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 768)  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,  
E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,  
J., Danzig,J. and Ducar,M.  
TITLE Creation of genome-wide protein expression libraries using random  
activation of gene expression  
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
MEDLINE 21227151  
COMMENT Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scaine@atersys.com  
High quality sequence stop: 469.  
FEATURES  
Source location/Qualifiers  
1..768  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, In press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."  
BASE COUNT 197 a 188 c 171 g 212 t  
ORIGIN  
Alignment Scores: 8.52e-153 Length: 768  
Pred. No.:

Score: 153.00 Matches: 153  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 80.53% Indels: 0  
DB: 12 Gaps: 0  
US-09-895-298a-83 (1-190) x Bg194960 (1-768)  
QY 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20  
|||||  
Db 85 ATGATGAATTTTCACCTCCGAGCAAGAGCTGGCGGCTCCACAGATGATGATCTTTCTTC 144  
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40  
|||||  
Db 145 ATCTTCTTCTCTTTTTCCTCATCTTCACCGGGGCTTGTGACCCCTGGCCATCACATC 204  
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60  
|||||  
Db 205 TGGAGATTGAAAGCCCTTCACCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 264  
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80  
|||||  
Db 265 TCCATCTACAGCTGGATGCACACCTTAAGTACACGCGCTGGCTACCTGTGGGTGTGG 324  
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100  
|||||  
Db 325 ATCTATCGAACCCTATTGGAAGTGTGCACTTCTTTTATCTCATCTCATTTGGCTTA 384  
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgLysIleMetIleArgLeuLeu 120  
|||||  
Db 385 ATCATCATCCTATCTTTACTGCGAGATCACAGAGGAGAGAAATATGATTAAGGCTGCTC 444  
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140  
|||||  
Db 445 CATGAGCAGATCATTAATGAGGCAAGATTAATGTTCTCTATGAAAAATGTATGATCAG 504  
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeu 153  
|||||  
Db 505 CTGCAGAGATATGAGAGAAAGCAACCCACCTCATCT 543  
RESULT 4  
Bg219307 822 bp mRNA linear EST 21-APR-2001  
LOCUS Bg219307  
DEFINITION RST93061 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION Bg219307  
VERSION Bg219307.1 GI:13745328  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 822)  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,  
E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,  
J., Danzig,J. and Ducar,M.  
TITLE Creation of genome-wide protein expression libraries using random  
activation of gene expression  
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
MEDLINE 21227151  
COMMENT Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scaine@atersys.com  
High quality sequence stop: 473.  
FEATURES  
Source location/Qualifiers  
1..822  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"

```
/cell_line="HT1080"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT      241 a      169 c      179 g      230 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:      2 01e-147      Length:      822
Score:          148.00      Matches:      148
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      77.89%      Indels:      0
DB:              12      Gaps:      0

US-09-895-298a-83 (1-190) x BG219307 (1-822)

QY      43      LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheLeuHisSerIle 62
      |||||||
Db      79      TTGAAGCCTTCAGCTGACGTGGCCCTTTCGAGGCTGCTCCTTCATTCACCTCATC 138

QY      63      TyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyr 82
      |||||||
Db      139      TACAGCGTGCATGCACACCCCTAGTACACGGCTGGCTACCTGGGCTTGTGGATCTAT 198

QY      83      ArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValIleIleIle 102
      |||||||
Db      199      CGGAACCTCTTTGGAAATGTGCACCTTTTTCATCTCTCACCCCTCATTTGGCTTAATCATC 258

QY      103      ThrTyrLeuTyrTrpGlnIleThrGlnGlyArgLysIleMetIleArgLeuLeuHisGln 122
      |||||||
Db      259      ACCTATCTTACAGCAGATCACAGAGGAAGATATATATAGCTGCTCATCAGAG 318

QY      123      GlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLysLeuGln 142
      |||||||
Db      319      CAGATCTATATATAGGCAAGATAAATATCTCTGATATAAATAATGATCAAGCTGACAG 378

QY      143      AspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGlnValGln 162
      |||||||
Db      379      GARTGTGAGAGAAAGAAAGCAAGCCAGCTCAGCTTGTGAAAAGAGAGAGGTGGACCA 438

QY      163      GlnGlyPheLeuHisLeuGlnGlyLysAspGlySerLeuAspLeuArgSerArgArgSer 182
      |||||||
Db      439      CAAGGCTTTTTCGATTTGGGGGAACATGATGCGATCTTGACCTTGCGATCTAGAAATCA 498

QY      183      ValGlnGlnGlyLysAsnProArgAla 190
      |||||||
Db      499      GTTCAAGAAAGTATATCCAAAGGCC 522

RESULT 5
LOCUS      BG221275      789 bp      mRNA      linear      EST 21-APR-2001
DEFINITION RST41079 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG221275
VERSION      BG221275.1      GI:13747296
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE      1 (bases 1 to 789)
AUTHORS      Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Kliska,A., Hess,J., Cochran,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE      Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL      Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE      21227151
```

```
COMMENT      Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 533.
Location/Qualifiers
1. 789
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT      191 a      194 c      171 g      226 t      7 others
ORIGIN

Alignment Scores:
Pred. No.:      3.3e-128      Length:      789
Score:          130.00      Matches:      130
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      68.42%      Indels:      0
DB:              12      Gaps:      0

US-09-895-298a-83 (1-190) x BG221275 (1-789)

QY      10      AlaTrpArgAlaSerGlnMetMetThrPhePheIlePheLeuLeuPhePheProSerPhe 29
      |||||||
Db      215      GCGTGGGGGCGTCACAGATGATGACTTCTTCATCTTCTGCTCTTTCGCCATCCTTC 274

QY      30      ThrGlyValLeuGlySerThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCys 49
      |||||||
Db      275      ACCGGGCTCTTGTGCACCCCGGCATCACCATCTGGAGATTGAAGCCTTACGCTGACTGT 334

QY      50      GlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeu 69
      |||||||
Db      335      GGGCCCTTTTGGAGGTGCTGCTCTTCATTCATCCATCTACAGCTGGATCGACACCTTA 394

QY      70      SerThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerVal 89
      |||||||
Db      395      AGTACACGGCCGCTGACCTGCTGGGTGTGGATCATCGAAGCCTCATTTGGAAGTGTG 454

QY      90      HisPhePhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIle 109
      |||||||
Db      455      CACTTCTTTTTCATCCCTCACCCCATTTGTCTATCATCACTATCTTTTACTGGCAGATC 514

QY      110      ThrGlnGlyArgLysIleMetIleArgLeuLeuHisGlnGlnIleIleAsnGlnGlyLys 129
      |||||||
Db      515      ACGAGAGGAGAGAGATTAATGATTAAGCTCTCTCATGACGACATCATTAATGAGGCCAA 574

QY      130      AspLysMetPheLeuIleGlnLysLeuIle 139
      |||||||
Db      575      GATAAATGTTCTCGATAGAAAATTTGATC 604

RESULT 6
LOCUS      BG183902      823 bp      mRNA      linear      EST 21-APR-2001
DEFINITION RST2815 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG183902
VERSION      BG183902.1      GI:13705589
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE      1 (bases 1 to 823)
AUTHORS      Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
```

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
21227151  
JOURNAL MEDLINE  
COMMENT  
Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scaine@atersys.com  
High quality sequence stop: 449.  
Location/Qualifiers  
1. 823  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."  
BASE COUNT 211 a 203 c 180 g 229 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 7.58e-123 Length: 823  
Score: 125.00 Matches: 125  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.79% Indels: 0  
DB: 12 Gaps: 0  
US-09-895-298A-83 (1-190) x BG183902 (1-823)  
QY 1 MetMetAsnPhgInProProSerIysAlaTrpArgAlaSerGlnMetThrPhePhe 20  
DB 109 ATGATGAATTTCCACGCTCCGAGCAAGCCTGGCGGCTCAGATGATGACTTCTTC 168  
QY 21 IlePheLeuPhePheProSerPheThrGlyValLeuCysThrIleuAlaIleThrIle 40  
DB 169 ATCTTCTGCTCTTTTCCATCTTCACCGGGGCTGTGTGACCCCTGGCCATCACCATC 228  
QY 41 TrpArgLeuPheProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60  
DB 229 TGGAGATTGAACCTTCAGCTGCTGCTTTTCGAGGCTGCTGCTTCTTCATTTCAC 288  
QY 61 SerIleYrSerTrpIleAspThrLeuSerThrArgProGlyIleuTrpValValTrp 80  
DB 289 TCATCTACAGCTGATGCACACCTAAGTACAGCGCTGGCTGAGGTTGTTGG 348  
QY 81 IleTrpArgAsnLeuIleGlySerValHisPhePhePheIleuThrIleuValLeu 100  
DB 349 ATCTATCGGAACCTATGGAGTGGAGCTCTTTTATCTTCACCTCATTTGGTGA 408  
QY 101 IleIleThrTrpLeuTrpGlnIleThrGlnGlyArgGlyIleuMetIleArgLeuLeu 120  
DB 409 ATCATCACTATCTTACTGCGAGATACAGAGGAGAAATTTATGATTAAGCTGCTC 468  
QY 121 HisGlnGlnIleIle 125  
DB 469 CATGAGACAGATCATC 483  
RESULT 7  
LOCUS BG216071 837 bp mRNA linear EST 21-APR-2001  
DEFINITION R5735885 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG216071

VERSION BG216071.1 GI:13742220  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS  
1 (bases 1 to 837)  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
21227151  
JOURNAL MEDLINE  
COMMENT  
Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scaine@atersys.com  
High quality sequence stop: 537.  
Location/Qualifiers  
1. 837  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."  
BASE COUNT 208 a 209 c 184 g 235 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.06e-120 Length: 837  
Score: 123.00 Matches: 123  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.74% Indels: 0  
DB: 12 Gaps: 0  
US-09-895-298A-83 (1-190) x BG216071 (1-837)  
QY 39 ThrIleTrpArgLeuPheProSerAlaAspCysGlyProPheArgGlyLeuProLeuPhe 58  
DB 238 ACCATCTGGAGATTGAACCTTCAGCTGCTGCTTTTCGAGGCTGCTGCTTCTTC 297  
QY 59 IleHisSerIleYrSerTrpIleAspThrLeuSerThrArgProGlyIleuTrpVal 78  
DB 298 ATTCACCTCATCTACAGCTGATGCACACCTTAAGTACAGCGCTGGCTGAGCTG 357  
QY 79 ValTrpIleTrpArgAsnLeuIleGlySerValHisPhePhePheIleuThrIleuVal 98  
DB 358 GTTGGATGATATCGGAACCTCATTTGGAAGTGGACCTCTTTTATCTTCACCTCAT 417  
QY 99 ValLeuIleIleThrTrpLeuTrpGlnIleThrGlnGlyArgGlyIleuMetIleArg 118  
DB 418 GTGCTAATGATCACTATCTTACTGCGAGATACAGAGGAGAAAGATTAAGATAAG 477  
QY 119 LeuLeuHisGlnGlnIleIleAsnGlnGlyIleAspIleuMetPheLeuIleGlyLeu 138  
DB 478 CTGCTCATGAGAGATCATTAATGAGGCAAAAGATAAATGTTCTGTAGAAAATTG 537  
QY 139 IleIleLeuGlnAspMetGlyIleIleAsnProSerSerIleuValLeuGlnGlnArg 158  
DB 538 ATCAAGCTTCAGGATATGGAGAAAGCAAAACCCAGCTCACTTGTCTGAAAAGAGA 597  
QY 159 GluValGlu 161

```

Db      598 GAGGTGAG 606
|||||
RESULT 8
LOCUS   BG982234/c
DEFINITION CM4-CN0089-130201-723-e04 CN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG982234
VERSION   BG982234.1 GI:14384969
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 447)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL Contact: Simpson A.J.G.
MEDLINE Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Brazil Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM4&t2=CM4-CN0089-
130201-723-e04&t3=2001-02-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 447.
FEATURES
    source
        1..447
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="CN0089"
            /rev_start="Adult"
            /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT 114 a 107 c 95 g 131 t
ORIGIN
Alignment Scores:
Pred. No.: 3,1e-109 Length: 447
Score: 112.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.95% Indels: 0
DB: 13 Gaps: 0
US-09-895-298a-83 (1-190) x BG982234 (1-447)
QY 79 ValTTP11eTyrARgsAnleuIllegIySerValHisPhePheIleuThrIleu 98
|||||
Db 380 GTTGGATCATCGAACCATCGAAGTCGACACTCTTTTCATCCACCCATAT 321
|||||
QY 99 ValLeuIleIleThyTyrIleuTyrTTPGlnIleThrGluGlyArgIysIleMetIleArg 118
|||||
f Db 320 GTCTATCATCATCACTATCTTACTGCGACAGATCAGAGGAGGAAGATTATGATAGG 261
|||||

```

```

QY 119 LeuLeuHisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLys 138
|||||
Db 260 CTGCTCCATGACGACATCATTAATGAGCGCAAGCATAAATGTTCCGATAGAAAATTG 201
|||||
QY 139 IleLysLeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValIleGluArg 158
|||||
Db 200 ATCAAGCTGCAGATATGAGAAAGAAAGCAAAACCCACGTCACCTGTTCTGGAAGGAGA 141
|||||
QY 159 GluValGluGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArg 178
|||||
Db 140 GAGGTGAGCAACAGGCTTTTGCATTTGGGCAACATATGCGACGTCTTGACTTCCGA 81
|||||
QY 179 SerArgSerValGlnGlnGluGlyAsnProArgAla 190
|||||
Db 80 TCTAGAAATCATCTCAAGAAAGTAATCCAAAGGCC 45
|||||
RESULT 9
LOCUS   AM469181/c
DEFINITION h078f11.x1 NCI-CGAP Gas4 Homo sapiens cDNA clone IMAGE:2898861 3'
similar to TR:043284 O43284 LAK-4P.;, mRNA sequence.
ACCESSION AM469181
VERSION   AM469181.1 GI:7039287
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 594)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNT at:
www.bio.lnsl.gov/dbp/image/image.html
Seq primer: -40UP from Glibco
High quality sequence stop: 404.
FEATURES
    source
        1..594
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="IMAGE:2898861"
            /clone_lib="NCI-CGAP_Gas4"
            /tissue_type="poorly differentiated adenocarcinoma with
            signal ring cell features"
            /lab_host="DH10B"
            /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.69 kb. Life Technologies catalog #:
            11549-011"
BASE COUNT 161 a 139 c 108 g 186 t
ORIGIN
Alignment Scores:
Pred. No.: 5,73e-107 Length: 594
Score: 110.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.89% Indels: 0
DB: 10 Gaps: 0
US-09-895-298a-83 (1-190) x AM469181 (1-594)
QY 81 IleTyrARgsAnleuIllegIySerValHisPhePheIleuThrIleuValIleu 100
|||||

```



|||||  
Db 582 ATCATCGGAACCTCATGGAAGTGTGCACCTCTTTTCACCTCACCCTATTTGCTGA 523  
Qy 101 I|e|l|e|t|t|t|y|r|e|u|t|t|p|g|l|n|l|e|t|t|t|g|l|y|a|g|l|y|l|e|t|t|e|l|e|a|g|l|e|u 120  
Db 522 ATCATCGGAACCTCATGGAAGTGTGCACCTCTTTTCACCTCACCCTATTTGCTGA 463  
Qy 121 H|s|g|l|u|g|l|n|l|e|a|s|g|l|y|l|y|a|s|p|l|y|s|e|t|t|p|h|e|u|l|e|g|l|u|l|y|e|u|l|e|y|s 140  
Db 462 CATGAGCAGATCATTAATGAGGCGCAAGATTAATGTTCTGATGAAATAATGATCAAG 403  
Qy 141 LeuGlnAspMetGluLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160  
Db 402 CTGCGAGATGATGAGAAAGCAAGCAAGCCAGCTCAGTCTGTTCTGGAAGGAGAGAGGTG 343  
Qy 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180  
Db 342 GAGCAACAAGGCTTTTTCATTTGGGCGACATGATGAGCTGAGCTTGCATCTGATCTAGA 283  
Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190  
Db 282 AGATCAGTTCAAGAGATATCCAAAGGCC 253  
RESULT 10  
Bg217799 777 bp mRNA linear EST 21-APR-2001  
LOCUS R373713 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION Bg217799  
VERSION Bg217799.1 GI:13743820  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 777)  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith,  
E., Veloso,N., Kijka,A., Hess,J., Cothen,K., Lo,K., Offenbacher,  
J., Danzig,J. and Ducar,M.  
TITLE Creation of genome-wide protein expression libraries using random  
activation of gene expression  
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
MEDLINE 21227151  
COMMENT Contact: Scott J. Cain  
Athensys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athensys.com  
High quality sequence stop: 512.  
Location/Qualifiers  
1. 777  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athensys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."  
BASE COUNT 196 a 193 c 173 g 214 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 5.9e-93 Length: 777  
Score: 97.00 Matches: 178  
Percent Similarity: 98.89% Conservative: 0  
Best Local Similarity: 98.89% Mismatches: 1  
Query Match: 51.05% Indels: 2  
DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x Bg217799 (1-777)  
Qy 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetRhphe 20  
Db 85 ATGATGAATTTCCACCTCCGAGCAAGCCTGGCGGCTCCACAGATGATGATCTTCTTC 144  
Qy 21 I|e|p|e|l|e|u|e|P|h|e|P|r|o|S|e|r|P|h|e|t|t|g|y|a|l|e|u|C|y|t|t|h|e|u|a|l|e|t|t|e 40  
Db 145 ATCTTCTTGCCTTTTCCATCTTCCATCCGAGGCGGCTTGTGTGACCCCTGACCACTAC 204  
Qy 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheLeu 60  
Db 205 TCGAATTTGAACCTTCTACCTGCTGCTGCTTTTCCAGGCTGCTGCTTCTTCACTTAC 264  
Qy 61 SerIleYSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80  
Db 265 TCCATCTACAGCTGTGATGACACCTTAAGTACACGCGCTGCTGCTGCTGCTGCTGCT 324  
Qy 81 I|e|t|y|r|a|g|a|s|p|l|e|u|l|e|g|y|s|e|r|v|a|l|n|s|p|h|e|p|h|e|l|e|u|t|t|h|e|u|l|e 100  
Db 325 ATCTATCGGAACCTCATGGAAGTGTGCACCTTTTTCATCTCACCCTCACC-TCGTCT 383  
Qy 100 u|l|e|l|e|t|t|t|y|r|e|u|t|t|p|g|l|n|l|e|t|t|t|g|l|y|a|g|l|y|l|e|t|t|e|l|e|a|g|l|e|u 120  
Db 384 ATCATCAACCTCATCTTCTTCTGCGACATGATCAGAGGAGGAGATTAATGATAGGCTGCT 443  
Qy 120 u|H|s|g|l|u|g|l|n|l|e|a|s|g|l|y|l|y|a|s|p|l|y|s|e|t|t|p|h|e|u|l|e|g|l|u|l|y|e|u 140  
Db 444 CCATGAGCAGATCATTAATGAGGCGCAAGATTAATGTTCTGATGAAATAATGATCA 503  
Qy 140 s|l|e|u|g|l|n|s|p|m|e|t|g|l|u|l|y|s|a|l|a|s|n|p|r|o|s|e|r|s|e|r|l|e|u|l|e|u|g|l|u|a|r|g|l|u|a 160  
Db 504 GCTGCAAGATGATGAGAAAGCAAGCAAGCCAGCTCAGTCTGTTCTGGAAGGAGAGGT 563  
Qy 160 I|g|l|u|g|l|n|g|l|n|g|l|y|p|h|e|u|n|s|l|e|u|g|l|y|l|u|n|s|a|s|p|g|l|y|s|e|r|l|e|u|a|s|p|l|e|u|a|r|g|s|e|r 179  
Db 564 GGAGCAACAAGGCTTTTTCATTTGGGCGGACATGATGAGCTTGCATCTTGCAGACT 621  
RESULT 11  
Bg375244 698 bp mRNA linear EST 24-NOV-2000  
LOCUS QV4-ST0212-261199-045-c09 ST0212 Homo sapiens cDNA, mRNA sequence.  
DEFINITION Bg375244  
ACCESSION Bg375244  
VERSION Bg375244.1 GI:11337269  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 698)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV4&cl2=QV4-ST0212-  
261199-045-c09&cl3=1999-11-26&cl4=1)



**AUTHORS** Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kliska, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.

**TITLE** Creation of genome-wide protein expression libraries using random activation of gene expression

**JOURNAL MEDLINE** Nat. Biotechnol. 19 (5), 440-445 (2001)

**COMMENT** Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9536  
Email: scaine@atersys.com  
High quality sequence stop: 307.

**FEATURES** source  
Location/Qualifiers

1. 307  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone.lib="Athersys RAGE library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

**BASE COUNT** 58 a 98 c 56 g 93 t

**ORIGIN**

**Alignment Scores:**

Pred. No.:	8,366-69	Length:	307
Score:	74.00	Matches:	74
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	38.95%	Indels:	0
DB:	12	Gaps:	0

US-09-895-298a-83 (1-190) x BG187692 (1-307)

**QY** 1 MetMetAsnPhenGlnProProSerLysAlaTTPArgAlaSerGlnMetThrPhe 20  
|||||  
**DB** 85 ATGATGAATTTCCAGCTCCGAGCAAGAGCTGGCGGCTCACAGATGATGACTTCTTC 144  
|||||  
**QY** 21 TlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40  
|||||  
**DB** 145 ATCTTCTTGTCTTTTCCATCCATCCACCGGGGCTCCTGTCACCCCTGGCATCACCATC 204  
|||||  
**QY** 41 TTPArgLeuLysProSerAlaAspGlyProPheArgGlyLeuProLeuPheIleHis 60  
|||||  
**DB** 205 TGGAGATTGAGAGCTTCACTGACTGAGTGGCCCTTTTGGAGGTCTGCTCTTCATTCCAC 264  
|||||  
**QY** 61 SerIleTyrSerTrpIleAspTrpIleuSerThrArgProGly 74  
|||||  
**DB** 265 TCATCTACAGCTGAGATCGACACCCCTAAGTACAGCGCTGC 306  
|||||  
**RESULT 14** B0084432 415 bp mRNA linear EST 04-APR-2002  
**LOCUS** B0084432  
**DEFINITION** K-EST0149711 S14K402 Homo sapiens cDNA clone S14K402-77-A05 5',  
**ACCESSION** B0084432  
**VERSION** B0084432.1 GI:19944432  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE** 1 (bases 1 to 415)  
**AUTHORS** Kim, N.-S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

**TITLE** 21C Frontier Korean EST Project 2001  
**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@email.kr.ibm.re.kr  
Plate: 77 row: A column: 05  
High quality sequence stop: 415.

**FEATURES** source  
Location/Qualifiers

1. 415  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone.lib="S14K402-77-A05"  
/clone.lib="S14K402"  
/cell\_line="K402"  
/lab\_host="Top10F"  
/note="Organ: Stomach; Vector: pTZ19Bp1; Site: 1: EcoRI; Site: 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

**BASE COUNT** 136 a 74 c 101 g 104 t

**ORIGIN**

**Alignment Scores:**

Pred. No.:	2,166-64	Length:	415
Score:	70.00	Matches:	70
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	36.84%	Indels:	0
DB:	14	Gaps:	0

US-09-895-298a-83 (1-190) x B0084432 (1-415)

**QY** 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetHleuIleGlnLysLeuIleLys 140  
|||||  
**DB** 1 CATGAGCAGATCATTAATGAGGCGCAAGATGTAATGTTCTCGATGAGAAATGATCAG 60  
|||||  
**QY** 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnUArgGlnVal 160  
|||||  
**DB** 61 CTGAGAGATATGGAAGAAAGCAACCCGCTCACTTGTCTTGGAAAGAGAGAGTG 120  
|||||  
**QY** 161 GlnGlnGlnGlyPheLeuHisLeuGlyGlnHisAspLysSerLeuAspLeuArgSerArg 180  
|||||  
**DB** 121 GAGCAACAAGCTTTTTCATTTGGGGGAAATGATGCAATCTGACTTCGATCTGAGA 180  
|||||  
**QY** 181 ArgSerValGlnGlnGlyAsnProArgAla 190  
|||||  
**DB** 181 AGATCAGTTCAGAAAGATATCCAAAGGCC 210  
|||||  
**RESULT 15** BM773483 482 bp mRNA linear EST 04-MAR-2002  
**LOCUS** BM773483  
**DEFINITION** K-EST0057945 S14K402 Homo sapiens cDNA clone S14K402-27-D11 5',  
**ACCESSION** BM773483  
**VERSION** BM773483.1 GI:19103098  
**KEYWORDS** EST.  
**SOURCE** human.

## ORGANISM

Homo sapiens

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 482)  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.

TITLE  
JOURNAL  
COMMENT

21C Frontier Korean EST Project 2001  
Unpublished (2002)  
Contact: Kim YS

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-350-4409  
Email: yongsung@email.krdb.re.kr  
Plate: 27 row: D column: 11  
High quality sequence stop: 482.

## FEATURES

## SOURCE

1..482  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="SI4K402-27-D11"  
/clone\_id="SI4K402"  
/cell\_line="K402"  
/lab\_host="Top10F"  
/note="Organ: Stomach; Vector: pTZ19BP1; Site\_1: EcoRI;  
Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tobacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F' by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

BASE COUNT 164 a 83 c 112 g 123 t  
ORIGIN

## Alignment Scores:

Pred. NO.: 2.52e-64 Length: 482  
Score: 70.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.84% Indels: 0  
DB: 14 Gaps: 0

US-09-895-298A-83 (1-190) x BM773483 (1-482)

OY 121 HISGLUGLIIELLEASNGIUGLYSASPLYSMETPHELEUILEGILUSYLEUILEYS 140  
DB 1 CATGAGCAGATCATTTAATGAGGCAAGATAAATTTCTGATAGAAAATTGATCAAG 60  
OY 141 LEUGINASPMEGLULYSLSALASNPSESRLEUVALLEUGIUAARGGIUVAL 160  
DB 61 CTGCAGGATATGAGAGAAAGCAAAACCCACGCTCACTGTTCTGGAAGAGAGAGCTG 120  
OY 161 GIUGINGINGIYPHELEUISTLEUGIUNHISAPGLYSERLEUASPLEUARGSERARG 180  
DB 121 GAGCAACAAGAGCTTTTTCATTTGGGGGAAACATGATGGACGTCTTGACTTGGCATCTAGA 180  
OY 181 ARGSEVALGINGIUGIYASNPFOARGALA 190  
DB 181 AGATCAGTTCAAGAGGATATTCACAGGGCC 210

Job time : 2214 secs